

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: MOGEN International nv
(B) STREET: Einsteinweg 97
(C) CITY: Leiden
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): 2333 CB
(G) TELEPHONE: 31-(0)71-5258282
(H) TELEFAX: 31-(0)71-5221471

(A) NAME: Gist-brocades N.V.
(B) STREET: Postbus 1
(C) CITY: Delft
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): 2600 MA
(G) TELEPHONE: 31-(0)15-2799111
(H) TELEFAX: 31-(0)15-2793957

(ii) TITLE OF INVENTION: Improved process for the production of
alcoholic beverages using Maltseed

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 96202195.2
(B) FILING DATE: 05-AUG-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..558

(D) OTHER INFORMATION: /product= "mature protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

5
ATG AGC GCG GGA ATC AAC TAC GTC CAG AAC TAC AAT GGC AAC CTC GGC 48
Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly
1 5 10 15

10
GAC TTT ACT TAC GAC GAG TCA GCG GGA ACT TTC AGC ATG TAT TGG GAG 96
Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu
20 25 30

15
GAT GGC GTG TCC TCA GAC TTC GTC GTG GGA CTG GGC TGG ACC ACT GGA 144
Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly
35 40 45

20
TCA TCC AAT GCG ATC ACC TAC AGC GCC GAG TAC TCC GCG TCA GGA TCA 192
Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
50 55 60

25
GCC TCC TAT CTG GCC GTG TAC GGA TGG GTG AAC TAC CCG CAG GCC GAG 240
Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
65 70 75 80

30
TAC TAC ATC GTG GAG GAT TAC GGA GAT TAC AAC CCA TGC AGC TCA GCG 288
Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
85 90 95

35
ACC TCC CTC GGA ACT GTG TAC AGC GAC GGC TCC ACC TAC CAG GTC TGC 336
Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
100 105 110

40
ACC GAC ACC CGC ACT AAC GAG CCG TCA ATC ACC GGC ACT TCC ACC TTC 384
Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
115 120 125

45
ACC CAG TAC TTC AGC GTG CGC GAG TCC ACT CGC ACC TCA GGA ACC GTG 432
Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
130 135 140

50
ACC GTC GCG AAC CAC TTC AAC TTC TGG GCG CAG CAC GGA TTC GGC AAC 480
Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn
145 150 155 160

55
AGC GAC TTT AAC TAC CAG GTG GTC GCA GTG GAG GCA TGG TCA GGA GCG 528
Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
165 170 175

60
GGC TCA GCG TCC GTC ACT ATC AGC TCC TG 558
Gly Ser Ala Ser Val Thr Ile Ser Ser
180 185

B4 (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ala | Gly | Ile | Asn | Tyr | Val | Gln | Asn | Tyr | Asn | Gly | Asn | Leu | Gly | 1 | 5 | 10 | 15 |
| Asp | Phe | Thr | Tyr | Asp | Glu | Ser | Ala | Gly | Thr | Phe | Ser | Met | Tyr | Trp | Glu | 20 | 25 | 30 | |
| Asp | Gly | Val | Ser | Ser | Asp | Phe | Val | Val | Gly | Leu | Gly | Trp | Thr | Thr | Gly | 35 | 40 | 45 | |
| Ser | Ser | Asn | Ala | Ile | Thr | Tyr | Ser | Ala | Glu | Tyr | Ser | Ala | Ser | Gly | Ser | 50 | 55 | 60 | |
| Ala | Ser | Tyr | Leu | Ala | Val | Tyr | Gly | Trp | Val | Asn | Tyr | Pro | Gln | Ala | Glu | 65 | 70 | 75 | 80 |
| Tyr | Tyr | Ile | Val | Glu | Asp | Tyr | Gly | Asp | Tyr | Asn | Pro | Cys | Ser | Ser | Ala | 85 | 90 | 95 | |
| Thr | Ser | Leu | Gly | Thr | Val | Tyr | Ser | Asp | Gly | Ser | Thr | Tyr | Gln | Val | Cys | 100 | 105 | 110 | |
| Thr | Asp | Thr | Arg | Thr | Asn | Glu | Pro | Ser | Ile | Thr | Gly | Thr | Ser | Thr | Phe | 115 | 120 | 125 | |
| Thr | Gln | Tyr | Phe | Ser | Val | Arg | Glu | Ser | Thr | Arg | Thr | Ser | Gly | Thr | Val | 130 | 135 | 140 | |
| Thr | Val | Ala | Asn | His | Phe | Asn | Phe | Trp | Ala | Gln | His | Gly | Phe | Gly | Asn | 145 | 150 | 155 | 160 |
| Ser | Asp | Phe | Asn | Tyr | Gln | Val | Val | Ala | Val | Glu | Ala | Trp | Ser | Gly | Ala | 165 | 170 | 175 | |
| Gly | Ser | Ala | Ser | Val | Thr | Ile | Ser | Ser | 180 | 185 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Nicotiana tabacum*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

AACTTCCTCA AGAGCTTCCC CTTTATGCC TTCCTTGTGTT TTGGCCAATA CTTGTAGCT 60

GTTACGCATG C 71

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCATGGCATG CGTAACAGCT ACAAAGTATT GGCCAAAACA AAGGAAGGCA TAAAAGGGGA 60

AGCTCTTGAG GAAGTTCATG 80

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGATGGCA TGCTGTTGTA G 21

B⁴
(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCACAATTCT CGAGGAGACC G

21

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCTCTTAAGG ATCCAATGCG G

21

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTTATCTGAA TTCGGAAGCT C

21